PATENTS

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Suzanne Cory, et al.	**Examiner**:	TO BE ASSIGNED
Serial No.:	TO BE ASSIGNED	**Art Unit:**	TO BE ASSIGNED
Filed:	Herewith	**Docket:**	11686a
For:	NOVEL MAMMALIAN GENE, BCL-W, BELONGS TO THE BCL-2 FAMILY OF APOPTOSIS-CONTROLLING GENES	**Date:**	August 9, 2001

Assistant Commissioner for Patents
United States Patent and Trademark Office
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Sir:

In connection with the filing of the above-identified application, kindly enter the following preliminary amendments.

In the specification:

Please insert the following text at page 1, line 3, underneath the title:

--**Cross-Reference to Related Application**

This application is a divisional of Serial No. 09/155,327, filed on March 29, 1999,

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CERTIFICATE OF MAILING BY "EXPRESS MAIL"

"Express Mail" Mailing Label Number: EL895322708US
Date of Deposit: August 9, 2001
I hereby certify that this Preliminary Amendment is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. §1.10 on the date indicated above and is addressed to the Assistant Commissioner of Patents and Trademarks, Washington, DC 20231.

Dated: August 9, 2001

_____
Janet Grossman

F: work\536\11686a\amend\11686a.pre

which was originally filed as International Application No. PCT/AU97/00199 on March 27, 1997.--

Please delete the Sequence Listing at pages 45-51 of the specification, and insert therefor the attached substitute copy of the Sequence Listing.

In the Drawings:

Please delete Figures 9A to 9B(iv) (drawing sheets 17/26 to 26/26), and replace therewith the attached substitute Figure 9A and Figure 9B.

In the Claims:

Please cancel claims 1-5 without prejudice.

REMARKS

The specification has been amended to add the cross reference to the parent application, Serial No. 09/155,327.

The Sequence Listing in the specification has been replaced with the attached substitute Sequence Listing. By way of the substitute Sequence Listing, Applicants have inserted the updated information with respect to the title of the invention and the prior application data. The sequences of SEQ ID NOS: 1 to 4 have been reformatted to conform with the sequence rules under 37 C.F.R. §1.821 with respect to unusual nucleotides and amino acid residues. In addition, Applicants have corrected certain clerical errors present in the original Sequence Listing.

More specifically, Applicants have corrected two clerical errors in the nucleotide sequence of SEQ ID NO: 6 (human bcl-w) at nucleotide position 301, 404 and 405. The protein sequence in SEQ ID NO: 7 has been amended to correct two clerical errors at positions 101 and 135. In addition, Applicants have corrected certain clerical errors in the nucleotide sequence of

SEQ ID NO: 8 (murine bcl-w) and in the protein sequence of SEQ ID NO: 9. These corrections are indicated in the attached marked-up copy of the Sequence Listing.

Applicants respectfully submit that the foregoing amendment does not introduce new matter. More specifically, the protein sequence of SEQ ID NO: 7 (human bcl-w) as amended is set forth in Figure 8 as originally filed. The protein sequence of SEQ ID NO: 9 (murine bcl-w) as amended is set forth in Figure 1 as originally filed. In addition, these protein sequences find support in Figures 9A and 9B of the priority document, Australian Provisional Application PN8965, filed on March 27, 1996. A courtesy copy of such priority document is enclosed for the Examiner's convenience (**Exhibit A**). The nucleotide sequences of SEQ ID NO: 6 and SEQ ID NO: 8 as amended are also disclosed in Figure 9A and 9B, respectively, of the priority document.

Applicants further respectfully submit that Figures 9A to 9B(iv), which set forth the nucleotide and protein sequences of human bcl-w and murine bcl-w, contain the same typographical errors as the original Sequence Listing. Accordingly, Applicants submit herewith substitute sheets of Figures 9A and 9B to replace the original drawing sheets of Figures 9A to 9B(iv). The substitute drawing of Figure 9B discloses the nucleotide sequence (SEQ ID NO: 6) and the encoded protein sequence (SEQ ID NO: 7) of human bcl-w. The substitute drawing of Figure 9B discloses the nucleotide sequence (SEQ ID NO: 8) and the encoded protein sequence (SEQ ID NO: 9) of murine bcl-w. These substitute sheets of drawings do not introduce new matter and are fully supported by the application as filed and by the priority document.

Applicants respectfully submit that the foregoing amendments do not introduce new subject matter.

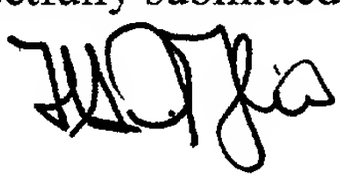
Claims 1-5 have been canceled without prejudice.

Attached hereto is a marked-up copy of the amendment to the specification and the claims, captioned "Version with Markings to Show Changes Made"; a substitute paper and an initial computer-readable copy of the Sequence Listing; a statement under §1.821(f) verifying that the content of the substitute paper copy and the initial computer-readable copy of the

Sequence Listing are the same; substitute sheets for Figures 9A and Figures 9B; and the priority document as Exhibit A.

It is respectfully submitted that the present case is in condition for allowance which action is earnestly solicited.

Respectfully submitted,



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Enclosures:
Version with Markings to Show Changes Made;
Substitute paper and initial computer-readable copy of the Sequence Listing;
Statement under §1.821(f);
Substitute sheets for Figures 9A and Figures 9B; and
Exhibit A.

Serial No.: TO BE ASSIGNED
Date: August 9, 2001

Version with Markings to Show Changes Made

In the Claims:

Claims 1-5 have been canceled.

In the Specification:

Please insert the following text at page 1, line 3, underneath the title:

--**Cross-Reference to Related Application**

This application is a divisional of Serial No. 09/155,327, filed on March 29, 1999, which was originally filed as International Application No. PCT/AU97/00199 on March 27, 1997.--

Please amend the Sequence Listing as follows (beginning on the next page).

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (Other than US) AMRAD OPERATIONS PTY LTD
(US only) Suzanne Cory, Jerry McKee Adams, Leonie Gibson and Sean P Holmgreen

(ii) TITLE OF INVENTION: ~~THERAPEUTIC MOLECULES~~ A Novel Mammalian Gene, bcl-w, belongs to the bcl-2 family of Apoptosis-controlling genes.

(iii) NUMBER OF SEQUENCES: 9

(iv) ~~CORRESPONDENCE~~ ADDRESS:
(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
~~(D) SOFTWARE: PatentIn Release #1.0, Version #1.25~~

(vi) ~~CURRENT~~ Prior APPLICATION DATA:
(A) APPLICATION NUMBER: ~~PCT INTERNATIONAL~~ 09/155,327
(B) FILING DATE: 27-MAR-1997

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PN 8965
(B) FILING DATE: 27-MAR-1996

(viii) A~~TTORNEY/AGENT INFORMATION:~~
(A) NAME: HUGHES DR, E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: +61 3 9254 2777
(B) T~~ELEFAX: +61 3 9254 2770~~

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTAGAAC TGGGGX(~~A/C~~)GX(~~A/G~~) TXGTXGCCTT X(~~C/T~~)TT 33
n h n r n n y
wherein n is inosine at position 16, 19, 22 and 25.

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa
Asn Trp Gly Arg (~~Ile/Val~~) Val Ala Phe Phe
5
wherein Xaa is Ile or Val.

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCCCA GCCXCCXT(~~C/T~~)X TCTTGGATCC A 31
n n k n
wherein n is inosine at position 14, 17 and 20.

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ile Gln (~~Asp/Glu~~) (~~Asn/Gln~~) Gly Gly Trp
Xaa 5 Xaa

wherein Xaa at position 4 is Asp or Glu, and Xaa at position 5 is Asn or Gln.

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val
5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC          48
Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
  1               5                  10                  15

TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC          96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
            20                  25                  30

CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA         144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
        35                  40                  45

GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG         192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
    50                  55                  60

GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC         240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65                  70                  75                  80

CAG GTC TCC GAC GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT         288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
                85                  90                  95

GTA GCC TTC TTT CTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC         336
Val Ala Phe Phe ~~Leu~~ Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
            100 Val             105                 110

AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC         384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
        115                 120                 125

TAC CTG GAG ACG CGG CTG GTG GAC TGG ATC CAC AGC AGT GGG GGC TGG         432
Tyr Leu Glu Thr Arg Leu ~~Val~~ Asp Trp Ile His Ser Ser Gly Gly Trp
    130                 135                 140

GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG         480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
145                 150                 155                 160

CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG         528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
                165                 170                 175

GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC         576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
            180                 185                 190

AAG TGA A                                                               583
Lys  *
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
1 5 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
85 90 95

Val Ala Phe Phe ~~Leu~~ Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
115 120 125

Tyr Leu Glu Thr Arg Leu ~~Val~~ Ala Asp Trp Ile His Ser Ser Gly Gly Trp
130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
180 185 190

Lys *

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
ATG GCG ACC CCA GCC TCA ACC CCA GAC ACA CGG GCT CTA GTG GCT GAC          48
Met ~~Pro~~ Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
 1  Ala             5                  10                  15

TTT GTA GGC TAT AGG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC          96
Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
            20                  25                  30

CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT         144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
        35                  40                  45

GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG         192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
    50                  55                  60

GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC         240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65                  70                  75                  80

CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG GGC CGT CTT         288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
                85                  90                  95

GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC         336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
            100                 105                 110

AAA GAA ATG GAG CCT TTG GTG GGA CAA GTG CAG GAT TGG ATG GTG GCC         384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp ~~Ile~~ Val Ala
        115                 120                 125 Met

TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGC GGC TGG         432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
    130                 135                 140

GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCA CGG         480
Ala ~~Asp~~ Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu ~~Asp~~ Ala Arg
145 Glu             150                 155         Glu     160

CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG         528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val ~~Ser~~ Thr Val Leu Thr Gly
                165                 170 Arg             175

GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC         576
```

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
180 185 190

AAG TGA 582
Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met ~~Pro~~ Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
1 5 10 15

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp ~~Ile~~ Met Val Ala
115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
130 135 140

Ala ~~Asp~~ Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu ~~Asp~~ Glu Ala Arg
145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala ~~Ser~~ Ser Val ~~Ser~~ Arg Thr Val ~~Val~~ Leu Thr Gly
165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
180 185 190

Lys